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1: Plant Cell 2002 Jun;14(6):1347-57

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Expression of the IRT1 metal transporter is controlled by metals at the levels of transcript and protein accumulation.

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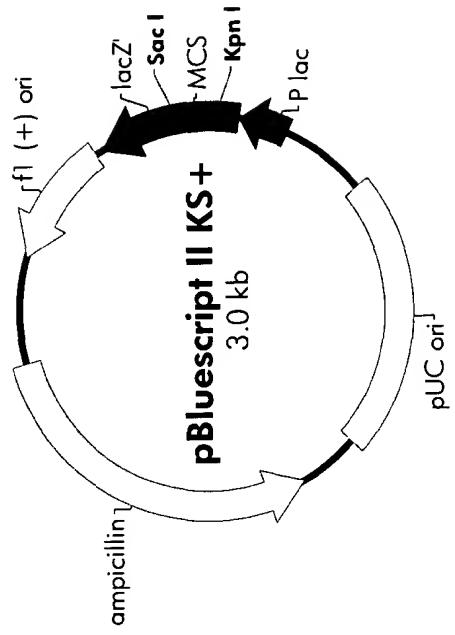
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Iron, an essential nutrient, is not readily available to plants because of its low solubility. In addition, iron is toxic in excess, catalyzing the formation of hydroxyl radicals that can damage cellular constituents. Consequently, plants must carefully regulate iron uptake so that iron homeostasis is maintained. The *Arabidopsis* IRT1 gene is the major transporter responsible for high-affinity iron uptake from the soil. Here, we show that the steady state level of IRT1 mRNA was induced within 24 h after transfer of plants to iron-deficient conditions, with protein levels peaking 72 h after transfer. IRT1 mRNA and protein were undetectable 12 h after plants were shifted back to iron-sufficient conditions. Overexpression of IRT1 did not confer dominant gain-of-function enhancement of metal uptake. Analysis of 35S-IRT1 transgenic plants revealed that although IRT1 mRNA was expressed constitutively in these plants, IRT1 protein was present only in the roots when iron is limiting. Under these conditions, plants that overexpressed IRT1 accumulated higher levels of cadmium and zinc than wild-type plants, indicating that IRT1 is responsible for the uptake of these metals and that IRT1 protein levels are indeed increased in these plants. Our results suggest that the expression of IRT1 is controlled by two distinct mechanisms that provide an effective means of regulating metal transport in response to changing environmental conditions.

PMID: 12084831 [PubMed - indexed for MEDLINE]

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- f1 (+) origin** 135–441
- β -galactosidase α -fragment** 460–816
- multiple cloning site** 653–760
- lac promoter** 817–938
- pUC origin** 1158–1825
- ampicillin resistance (*bla*) ORF** 1976–2833

pBluescript II KS (+/-) Multiple Cloning Site Region
(sequence shown 598-826)

The diagram illustrates the T7/T3 promoter region with two main promoter regions: T7 Promoter and T3 Promoter.

- T7 Promoter:** Located at the top. It contains a **M13-20 primer binding site** (underlined) and a **T7 primer binding site** (underlined). The sequence is: **TGTAAAACGACGCCAGTGGCGCGTAATACGACTCACTATAGGGCGAATTGGAGCTCCACCGGGCTCTAGA...**
- T3 Promoter:** Located at the bottom. It contains a **SK primer binding site** (underlined) and a **T3 primer binding site** (underlined). The sequence is: **...CAGCTTTGTTCCCTTAGTGAGGGTTAAATCATGGTCATAAGCTGTTTCC...**
- Restriction Sites:** Various restriction enzymes are indicated by vertical lines with labels: BssH II, Sma I, Pst I, EcoR I, EcoRV, Hind III, BspI 106 I, Cla I, Hinc II, Acc I, Sal I, Xba I, Eag I, Not I, BstX I, Sac II, Kpn I, Dra II, Apa I, EcoO 109 I.
- Primer Binding Sites:**
 - T7 primer binding site:** Located between positions 10 and 20 of the M13-20 sequence.
 - T3 primer binding site:** Located between positions 10 and 20 of the T3 sequence.
 - SK primer binding site:** Located between positions 10 and 20 of the T3 sequence.
 - M13 Reverse primer binding site:** Located between positions 10 and 20 of the M13-20 sequence.
 - KS primer binding site:** Located between positions 10 and 20 of the T3 sequence.
- α-fragment:** A bracket labeled "β-gal α-fragment" spans the region from position 10 to approximately 35 of the T3 sequence.
- β-gal fragment:** A bracket labeled "β-gal β-fragment" spans the region from position 10 to approximately 45 of the T3 sequence.